7.0   SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Ralph, David
                   An, Gang
                   O'Hara, Mark S.
                   Veltri, Robert

    (ii) TITLE OF INVENTION: DIAGNOSIS OF DISEASE STATE USING mRNA
           PROFILES IN PERIPHERAL LEUKOCYTES

  (iii) NUMBER OF SEQUENCES: 55

   (iv) CORRESPONDENCE ADDRESS:
        (A) ADDRESSEE: Arnold, White & Durkee
        (B) STREET: P.O. Box 4433
        (C) CITY: Houston
        (D) STATE: Texas
        (E) COUNTRY: USA
        (F) ZIP: 77210

    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

   (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: US Unknown
        (B) FILING DATE: Concurrently Herewith
        (C) CLASSIFICATION: Unknown

  (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: US 60/041,576
        (B) FILING DATE: 24-MAR-1997

 (viii) ATTORNEY/AGENT INFORMATION:
        (A) NAME: Nakashima, Richard A.
        (B) REGISTRATION NUMBER: P-42,023
        (C) REFERENCE/DOCKET NUMBER: UROC:014

   (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 387 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GGTGAGCCCC AGGAGACAGA AGAGATATGA GGAAATTGTT AAGGAAGTCA GCACTTACAT        60

TAAGAAAATT GGCTACAACC CCGACACAGT AGCATTTGTG CCAATTTCTG GTTGGAATGG       120

TGACAACATG CTGGAGCCAA GTGCTAACAT GCCTTGGTTC AAGGGATGGA AAGTCACCCG       180

TAAGGATGGC AATGCCAGTG GAACCACGCT GCTTGAGGCT CTGGACTGCA TCCTACCACC       240

AACTCGTCCA ACTGACAAGC CCTTGCGCCT GCCTCTCCAA GGATGTTCTT ACAAAATTGG       300

TGGTATTGGT ACTGTTCCCT GTTTGGCCGA ATTGGAAAAC TGGTGTTCCT CCAAACCCCG       360

GTTATGGTGG GTTTCCTCCT CCTTGGA                                          387
```

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 365 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
GGGCGGAACA AGGGAGCGCT AAAAGGAAAT TAGGATGTCA GGTGCATAAA GGACATAATT        60

CCAAAACCTT TCCAAACCCC AAATTTATTC AAAGGAACTG AGGAGTGGAT TGAGGAGTGG       120

ACCAACACTG GCGCCAAACA CAGAAATTAT TGTAAAGCTT TCTGATGGAA GAGAGCTCTG       180

TCTGGGCCCC AAGGAAAACT GGGTGCAGAG GGTTGTGGAG AAGTTTTTGA AGAGGGCTGA       240

GAATTCATAA AAAAATTCAT TCTCTGTGGT ATCCAAGAAT CAGTGAAGAT GCCAGTGAAA       300

CTTCAAGCAA ATCTACTTCA ACACTTCATG TATTGTGTGG GTCTGTTGTA GGGTTGCCAG       360

TTGTT                                                                 365
```

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 598 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
GCTTGGGCCC CAAGGAAAAC TGGGTGCAGA GGGTTGTGGA GAAGTTTTTG AAGAGGTAAG        60

TTATATATTT TTGAATTTAA AATTTGTCAT TTATCCGTGA GACATATAAT CCAAAGTCAG       120

CCTATAAATT TCTTTCTGTT GCTAAAAATC GTCATTAGGT ATCTGCCTTT TTGGTTAAAA       180

AAAAAAGGAA TAGCATCAAT AGTGAGTGTG TTGTACTCAT GACCAGAAAG ACCATACATA       240

GTTTGCCCAG GAAATTCTGG GTTTAAGCTT GTGTCCTATA CTCTTAGTAA AGTTCTTTGT       300

CACTCCCAGT AGTGTCCTAT GTTAGATGAT AATGTCTTTG ATCTCCCTAT TTATAGTTGA       360

GAATATAGAG CATGTCTAAC ACATGAATGT CAAAGACTAT ATTGACTTTT CAAGAACCCT       420

ACTTTCCTTC TTATTAAACA TAGCTCATCT TTATATTGTG AATTTTATTT TAGGGCTGAG       480

AATTCATAAA AAAATTCATT CTCTGTGGTA TCCAAGAATC AGTGAAGATG CCAGTGAAAC       540

TTCAAGCAAA TCTACTTCAA CACTTCATGT ATTGTGTGGG TCTGTTGTAG GGTTGCCA       598
```

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
CGCCTCAGGC TGGGGCAGCA TT        22
```

(2) INFORMATION FOR SEQ ID NO:5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACAGTGGAAG AGTCTCATTC GAGAT   25

(2) INFORMATION FOR SEQ ID NO:6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGAGCTGCCT GACGGCCAGG TCATC   25

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAAGCATTTG CGGTGGACGA TGGAG   25

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GACAACATGC TGGAGCCAAG TGC   23

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACCACCAATT TTGTAAGAAC ATCCT   25

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGCCCCAAG GAAAACT   17

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGGCAACCCT ACAACAGACC   20

(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGCCCCAAG GAAAACT   17

(2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACGACTCACT ATAAGCAGGA   20

(2) INFORMATION FOR SEQ ID NO:14:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGACCCAGCC CCTTGAGAAA CCT   23

(2) INFORMATION FOR SEQ ID NO:15:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCCTCAGGCT GGGGCAGCAT T   21

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTCACCTTC TGAGGGTGAA CTTGC   25

(2) INFORMATION FOR SEQ ID NO:17:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AACAACTGGC AA   12

(2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 12 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCGACAAGG AG   12

(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGAGCTGCCT GACGGCCAGG TCATC   25

(2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTGCCAAGGA GTGCTAAAGA AC   22

(2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 18 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGGACCCCAA GGAAAACT   18

(2) INFORMATION FOR SEQ ID NO:22:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 16 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGGCCCAAGG AAAACT   16

(2) INFORMATION FOR SEQ ID NO:23:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 20 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AACAGCTATG ACCATCGTGG   20

(2) INFORMATION FOR SEQ ID NO:24:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 20 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ACGACTCACT ATGTGGAGAA   20

(2) INFORMATION FOR SEQ ID NO:25:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTGGCCTACG GAAGATACGA CAC   23

(2) INFORMATION FOR SEQ ID NO:26:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ACAATCCGGA GGCATCAGAA ACT   23

(2) INFORMATION FOR SEQ ID NO:27:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGCCCCGGCC TCCTCGTCCT C   21

(2) INFORMATION FOR SEQ ID NO:28:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 19 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGCGGCGGCA GCGGTTCTC   19

(2) INFORMATION FOR SEQ ID NO:29:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1614 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```
GCGGCAGGCG CGGCAAATTA CGTTGCCGGA GCTGAACGGC GCGGCTGGTC TGAAGGCAAA      60

CAAGCGAGCG AGCGCGCGAT AGGGGCCGAG AGGACGCGCA GGTGGCGGCG TTGCCATGTC     120

GCACGGTCAC AGCCACGGCG GGGGTGGCTG CCGCTGCGCC GCCGAACGGG AGGAGCCGCC     180

CGAGCAGCGC GGCCTGGCCT ACGGCCTGTA CCTGCGCATC GACCTGGAGC GGCTGCAATG     240

CCTTAACGAG AGCCGCGAGG GCAGCGGCCG CGGCGTCTTC AAGCCATGGG AGGAGCGGAC     300

CGACCGCTCC AAGTTTATTG AAAGTGATGC AGATGAAGAG CTTCTGTTTA ATATTCCATT     360

TACGGGCAAT GTCAAGCTCA AAGGCATCAT TATAATGGGA GAGGATGATG ACTCACACCC     420

CTCTGAGATG AGACTGTACA AGAATATTCC ACAGATGTCC TTTGATGATA CAGAAAGGGA     480

GCCAGATCAG ACCTTTAGTC TGAACCGGGA TCTTACAGGA GAATTAGAGT ATGCTACAAA     540

AATTTCTCGT TTTTCAAATG TCTATCATCT CTCAATTCAT ATTTCAAAAA ACTTCGGAGC     600

AGATACGACA AAGGTCTTTT ATATTGGCCT GAGAGGAGAG TGGACTGAGC TTCGCCGACA     660

CGAGGTGACC ATCTGCAATT ACGAAGCATC TGCCAACCCA GCAGACCATA GGGTCCATCA     720

GGTTACCCCA CAGACACACT TTATTTCCTA AGGGCTGGCC AAGGCTCCCA TAGAGGCGCT     780

GTGTCAGTGA AGATGTACGA CTACCTGTTG GGAAGGACAA AGGGATGAGG CTCCAGAGAG     840

AGTTGGCTGC CACAGCTCTG CCAAGCTTTG TCTTTGGGGC TTGCTGCAGA AACCTGGCCT     900

ACGGAAGATA CGACACCACT GGGAGGGTTG TGTAGGTGCC AGGGGACCAT CGTGGTTCTC     960

TAGGGCGCTG TGGAAATTGG GTCTTGGGCT GGGTGGCATC TGGCAGTCAT GGGTAACACT    1020

TGCTTTTCCA GTTAATGTGG CCATGTGATT CCAAGTGTCA TGTTGCTTTG TGGAAGATTG    1080

TTGTGTGACT TGTTTTTTTG ATTTTGTATT TGTTTTTTTA AAGGAAACTA TTTGTGGGCT    1140

ATAGGAAACT TTCTGATGCC TCCGGATTGT GTTAGTAGTA GCCATCAGGA GGGTCTCCAA    1200

CTAAAACACT TGTTCCTGCT TGCTCCTTTC CCCTCTCATT GTTCAGCATT CTTGTCAAGT    1260

TGCCCAGCTT GGAGTTGTCT GTCACGCACA TGTGTCCTGT GGTTATAGCT AGAAGGACAG    1320
```

```
GAGTCTCCTG CTGATGCGTG ATAGCTTAAG CTTGGGGAGA AGGTCTTTTC CACTGCCTAG        1380

CTAAGCAGTC TGGGGAGAGC ATGGGGATCA TTTCTATGTG TGTGGGTAAT CTGGTCAGTA        1440

AGATTGAGAC TTAGTTAAGA TTCCCCTTGG AAATTCCTTA ATGTTTATTA GCTTCTAACT        1500

AGTGTTGTAA GTCCGATGCC AGAATTTGGA GATTTGAGTT CTTCTTTTCA TGGCTTTTAT        1560

TCACTGTGAC TAATAAGCTT CCTAATAAAT CCTTGCCAGA CTTAAAAAAA AAAA             1614
```
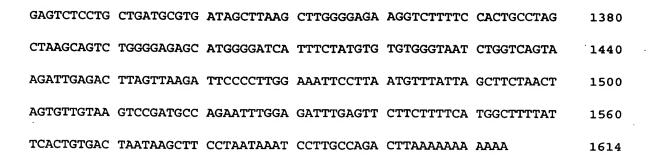
(2) INFORMATION FOR SEQ ID NO:30:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1268 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```
TTTCAAGCCG TGGGAGGACG GACCGACCGC TCCAAGTTCG CTGAAAGTGA TGCGGACGAA          60

GAGCTCCTGT TTAATATTCC GTTTACGTGC AATGTCAAGC TGAAAGGCGT CATCATAATG         120

GGCGAGGATG ATGACTCGCA CCCCTCGGAG ATGAGACTGT ACAAGAACAT TCCACAGATG         180

TCATTTGATG ACACAGAAAG GGAGCCAGAG CAGACCTTCA GTCTGAACCG AGACATTACA         240

GGAGAATTAG AATATGCTAC GAAAATCTCC AGGTTTTCAA ATGTCTATCA TCTTTCCATT         300

CATATTTCAA AAAACTTTGG AGCAGATACG ACGAAGATCT TTTATATTGG CCTGCGGGGA         360

GAGTGGACTG AGCTTCGCCG GCATGAGGTG ACCATCTGCA ACTATGAAGC GTCAGCCAAC         420

CCAGCAGACC ACCGGGTGCA TCAGGTCACC CCGCAGACAC ACTTCATTTC TTAAGGGCCA         480

GCCGGGGCTC CCTCAGATGC GCTGTTAGTG AAGATGTGCG ACCACCTGCT GGGAAGGACA         540

GAGGATGCTC CAGCAATAGT TGCCTGCCAG AGCTTTGGCC AGGCTTTGTC TCGGGGTTGC         600

TGCAGGAACC TGGCCTGTGG AAACCGCCTC ACCACCAGGA GCGGTATGGG TGCCAAGGGA         660

TAGTCTCTCT CTAAGGCACT GCAGAAACTG GGTCTTAGGC TGGGTGGCAT CTGTCAGTCA         720

TGAATAATGC TCACTTCCCA GTCTGTGGCC ACGGGATCCC ATGTGTCTTT TTGCTTGATT         780

TCTTGTGTGG TTTGTCCTTT TGTGGCATCA AAAAGGATGC TTCCTTGACC GTAGAATCCT         840

TCTGAAACCC GAGTTTCGTG TTTGAATTAG CCATCAGGAG GGTCTCCAGC TAGAAACACT         900

TCGTCCCTGC TTGCTCCTCC TCCTGTCATT GCTCAGCATT CGTGTCAGGG TGCCTAGCTG         960

GTGTCACATA TCAGACACAA GTGTCCCACA ATGGTGGTTG GAAAGGAAGG AGTCTCCTGA        1020
```

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```

A: 149107(UROC014P.DOC)
```

TACATGACTG CTTGGGGAAG GCTTACACAG TCTAGCCAAA TTAGTTGCGA GTCCTTTCCC   1080

TGTGTGGGTG ACCTGGTTGG GGTAAAACTG AGACAGTAAA GATTCCTCTT GGGACCTCCT   1140

TGGTGTTTCC CTGCTTCTAA CTCATGTTAT AAACCCAGGG CTGGAGTCTG GAGACCCTGC   1200

TCCTTCTGTT CATGGCTTTC ATTCATGGTG ACTAATGAGC TTCCTAATAA ATCCTTAGAG   1260

ACTTAAAA   1268

(2) INFORMATION FOR SEQ ID NO:31:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 211 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

     Met Ser His Gly His Ser His Gly Gly Gly Gly Cys Arg Cys Ala Ala
     1   5   10   15

     Glu Arg Glu Glu Pro Pro Glu Gln Arg Gly Leu Ala Tyr Gly Leu Tyr
                     20   25   30

     Leu Arg Ile Asp Leu Glu Arg Leu Gln Cys Leu Asn Glu Ser Arg Glu
                 35   40   45

     Gly Ser Gly Arg Gly Val Phe Lys Pro Trp Glu Glu Arg Thr Asp Arg
             50   55   60

     Ser Lys Phe Ile Glu Ser Asp Ala Asp Glu Glu Leu Leu Phe Asn Ile
     65   70   75   80

     Pro Phe Thr Gly Asn Val Lys Leu Lys Gly Ile Ile Ile Met Gly Glu
                     85   90   95

     Asp Asp Asp Ser His Pro Ser Glu Met Arg Leu Tyr Lys Asn Ile Pro
                     100   105   110

     Gln Met Ser Phe Asp Asp Thr Glu Arg Glu Pro Asp Gln Thr Phe Ser
             115   120   125

     Leu Asn Arg Asp Leu Thr Gly Glu Leu Glu Tyr Ala Thr Lys Ile Ser
             130   135   140

     Arg Phe Ser Asn Val Tyr His Leu Ser Ile His Ile Ser Lys Asn Phe
     145   150   155   160

     Gly Ala Asp Thr Thr Lys Val Phe Tyr Ile Gly Leu Arg Gly Glu Trp
                     165   170   175

                                   184

A: 149107(UROC014P.DOC)

```
Thr Glu Leu Arg Arg His Glu Val Thr Ile Cys Asn Tyr Glu Ala Ser
            180                 185                 190

Ala Asn Pro Ala Asp His Arg Val His Gln Val Thr Pro Gln Thr His
            195                 200                 205

Phe Ile Ser
    210
```

(2) INFORMATION FOR SEQ ID NO:32:

      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 157 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
Phe Lys Pro Trp Glu Glu Arg Thr Asp Arg Ser Lys Phe Ala Glu Ser
1               5               10                  15

Asp Ala Asp Glu Glu Leu Leu Phe Asn Ile Pro Phe Thr Cys Asn Val
            20                  25                  30

Lys Leu Lys Gly Val Ile Ile Met Gly Glu Asp Asp Ser His Pro
            35                  40                  45

Ser Glu Met Arg Leu Tyr Lys Asn Ile Pro Gln Met Ser Phe Asp Asp
    50                  55                  60

Thr Glu Arg Glu Pro Glu Gln Thr Phe Ser Leu Asn Arg Asp Ile Thr
65                  70                  75                  80

Gly Glu Leu Glu Tyr Ala Thr Lys Ile Ser Arg Phe Ser Asn Val Tyr
                85                  90                  95

His Leu Ser Ile His Ile Ser Lys Asn Phe Gly Ala Asp Thr Thr Lys
            100                 105                 110

Ile Phe Tyr Ile Gly Leu Arg Gly Glu Trp Thr Glu Leu Arg Arg His
        115                 120                 125

Glu Val Thr Ile Cys Asn Tyr Glu Ala Ser Ala Asn Pro Ala Asp His
        130                 135                 140

Arg Val His Gln Val Thr Pro Gln Thr His Phe Ile Ser
145                 150                 155
```

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(2) INFORMATION FOR SEQ ID NO:33:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 207 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
Cys Ser His Gly His Ser His Asn Cys Ala Ala Glu His Ile Pro Glu
1               5                   10                  15

Val Pro Gly Asp Asp Val Tyr Arg Tyr Asp Met Val Ser Tyr Ile Asp
            20              25                  30

Met Glu Lys Val Thr Thr Leu Asn Glu Ser Val Asp Gly Ala Gly Lys
            35              40                  45

Lys Val Phe Lys Val Met Glu Lys Arg Asp Asp Arg Leu Glu Tyr Val
            50              55              60

Glu Ser Asp Cys Asp His Glu Leu Leu Phe Asn Ile Pro Phe Thr Gly
65              70                      75                  80

His Val Arg Leu Thr Gly Leu Ser Ile Ile Gly Asp Glu Asp Gly Ser
            85                  90                  95

His Pro Ala Lys Ile Arg Leu Phe Lys Asp Arg Glu Ala Met Ser Phe
            100             105                 110

Asp Asp Cys Ser Ile Glu Ala Asp Gln Glu Ile Asp Leu Lys Gln Asp
            115             120                 125

Pro Gln Gly Leu Val Asp Tyr Pro Leu Lys Ala Ser Lys Phe Gly Asn
    130             135                 140

Ile His Asn Leu Ser Ile Leu Val Asp Ala Asn Phe Gly Glu Asp Glu
145             150                 155                 160

Thr Lys Ile Tyr Tyr Ile Gly Leu Arg Gly Glu Phe Gln His Glu Phe
                165                 170                 175

Arg Gln Arg Ile Ala Ile Ala Thr Tyr Glu Ser Arg Ala Gln Leu Lys
            180                 185                 190

Asp His Lys Asn Glu Ile Pro Asp Ala Val Ala Lys Gly Leu Phe
            195             200                 205
```

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(2) INFORMATION FOR SEQ ID NO:34:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3205 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```
CGACTCGTCG CCATTCCCGG AGCAGGTCGG CCTCGGCCCA GGGGCGAGTA TCCGTTGCTG      60

TGTCGGAGAC ACTAGTCCCC GACACCGAGA CAGCCAGCCC TCTCCCCTGC CTCGCGGCGG     120

GAGAGCGTGT CCGGCCGGCC GGCCGGCGGG GCTCGCGCAA CCTCCCTCGC CTCCCCTTCC     180

CCCGCAGCCT CCGCCCCGCC AGGCCCGGCC CGGACTCCCG AGCCCCGGCC TCCTCGTCCT     240

CGGTCGCCGC TGCCGCCGGG CTTAACAGCC CCGTCCGCCG CTTCTCTTCC TAGTTTGAGA     300

AGCCAAGGAA GGAAACAGGG AAAAATGTCG CCATGAAGGC CGAGAACCGC TGCCGCCGCC     360

GACCCCCGCC GGCCCTGAAC GCCATGAGCC TGGGTCCCCG CCGCGCCCGC TCCGCTCCGA     420

CTGCCGTCGC CGCCGAGGCC CCCGTTGATG CCGCTGAGCT CCCCCAACGC CGCCGCCACC     480

GCCTCCGACA TGGACAAGAA CAGCGGCTCC AACAGCTCCT CCGCCTCTTC GGGCAGCAGC     540

AAAGGGCAAC AGCCGCCCCG CTCCGCCTCG GCGGGGCCAG CCGGCGAGTC TAAACCCAAG     600

AGCGAATTAC TAATTTCAGC TGGATTCAAT TTGTTGTCAG TTGATTCTGT AGTAAGGCCA     660

TATGTTGCCC CTCTGGAGGT GCTTGTCAAC TACTCTGGAT GATGGATGGA AAGAACTCCA     720

GTGGATCCAA GCGTTATAAT CGCAAACGTG AACTTTCCTA CCCCAAAAAT GAAAGTTTTA     780

ACAACCAGTC CCGTCGCTCC AGTTCACAGA AAAGCAAGAC TTTTAACAAG ATGCCTCCTC     840

AAAGGGGCGG CGGCAGCAGC AAACTCTTTA GCTCTTCTTT TAATGGTGGA AGACGAGATG     900

AGGTAGCAGA GGCTCAACGG GCAGAGTTTA GCCCTGCCCA GTTCTCTGGT CCTAAGAAGA     960

TCAACCTGAA CCACTTGTTG AATTTCACTT TTGAACCCCG TGGCCAGACG GGTCACTTTG    1020

AAGGCAGTGG ACATGGTAGC TGGGGAAAGA GGAACAAGTG GGACATAAG CCTTTTAACA    1080

AGGAACTCTT TTTACAGGCC AACTGCCAAT TTGTGGTGTC TGAAGACCAA GACTACACAG    1140

CTCATTTTGC TGATCCTGAT ACATTAGTTA ACTGGGACTT TGTGGAACAA GTGCGCATTT    1200

GTAGCCATGA AGTGCCATCT TGCCCAATAT GCCTCTATCC ACCTACTGCA GCCAAGATAA    1260

CCCGTTGTGG ACACATCTTC TGCTGGGCAT GCATCCTGCA CTATCTTTCA CTGAGTGAGA    1320
```

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AGACGTGGAG TAAATGTCCC ATCTGTTACA GTTCTGTGCA TAAGAAGGAT CTCAAGAGTG 1380

TTGTTGCCAC AGAGTCACAT CAGTATGTTG TTGGTGATAC CATTACGATG CAGCTGATGA 1440

AGAGGGAGAA AGGGGTGTTG GTGGCTTTGC CCAAATCCAA ATGGATGAAT GTAGACCATC 1500

CCATTCATCT AGGAGATGAA CAGCACAGCC AGTACTCCAA GTTGCTGCTG GCCTCTAAGG 1560

AGCAGGTGCT GCACCGGGTA GTTCTGGAGG AGAAAGTAGC ACTAGAGCAG CAGCTGGCAG 1620

AGGAGAAGCA CACTCCCGAG TCCTGCTTTA TTGAGGCAGC TATCCAGGAG CTCAAGACTC 1680

GGGAAGAGGC TCTGTCGGGA TTGGCCGGAA GCAGAAGGGA GGTCACTGGT GTTGTGGCTG 1740

CTCTGGAACA ACTGGTGCTG ATGGCTCCCT TGGCGAAGGA GTCTGTTTTT CAACCCAGGA 1800

AGGGTGTGCT GGAGTATCTG TCTGCCTTCG ATGAAGAAAC CACGGAAGTT TGTTCTCTGG 1860

ACACTCCTTC TAGACCTCTT GCTCTCCCTC TGGTAGAAGA GGAGGAAGCA GTGTCTGAAC 1920

CAGAGCCTGA GGGGTTGCCA GAGGCCTGTG ATGACTTGGA GTTAGCAGAT GACAATCTTA 1980

AAGAGGGGAC CATTTGCACT GAGTCCAGCC AGCAGGAACC CATCACCAAG TCAGGCTTCA 2040

CACGCCTCAG CAGCTCTCCT TGTTACTACT TTTACCAAGC GGAAGATGGA CAGCATATGT 2100

TCCTGCACCC TGTGAATGTG CGCTGCCTCG TGCGGGAGTA CGGCAGCCTG GAGAGGAGCC 2160

CCGAGAAGAT CTCAGCAACT GTGGTGGAGA TTGCTGGCTA CTCCATGTCT GAGGATGTTC 2220

GACAGCGTCA CAGATATCTC TCTCACTTGC CACTCACCTG TGAGTTCAGC ATCTGTGAAC 2280

TGGCTTTGCA ACCTCCTGTG GTCTCTAAGG AAACCCTAGA GATGTTCTCA GATGACATTG 2340

AGAAGAGGAA ACGTCAGCGC CAAAAGAAGG CTCGGGAGGA ACGCCGCCGA GAGCGCAGGA 2400

TTGAGATAGA GGAGAACAAG AAACAGGGCA AGTACCCAGA AGTCCACATT CCCCTCGAGA 2460

ATCTACAGCA GTTTCCTGCC TTCAATTCTT ATACCTGCTC CTCTGATTCT GCTTTGGGTC 2520

CCACCAGCAC CGAGGGCCAT GGGGCCCTCT CCATTTCTCC TCTCAGCAGA AGTCCAGGTT 2580

CCCATGCAGA CTTTCTGCTG ACCCCTCTGT CACCCACTGC CAGTCAGGGC AGTCCCTCAT 2640

TCTGCGTTGG GAGTCTGGAA GAAGACTCTC CCTTCCCTTC CTTTGCCCAG ATGCTGAGGG 2700

TTGGAAAAGC AAAAGCAGAT GTGTGGCCCA AAACTGCTCC AAAGAAAGAT GAGAACAGCT 2760

TAGTTCCTCC TGCCCCTGTG GACAGCGACG GGGAGAGTGA TAATTCAGAC CGTGTTCCTG 2820

TGCCCAGTTT TCAAAATTCC TTCAGCCAAG CTATTGAAGC AGCCTTCATG AAACTGGACA 2880

CACCAGCTAC TTCAGATCCC CTCTCTGAAG AGAAAGGAGG AAAGAAAAGA AAAAAACAGA 2940

188

AACAGAAGCT CCTGTTCAGC ACCTCAGTCG TCCACACCAA GTGACACTAC TGGCCCAGGC   3000

TACCTTCTCC ATCTGGTTTT TGTTTTTGTT TTTTTTTCCC CCATGCTTTT GTTTGGCTGC   3060

TGTAATTTTT AAGTATTTGA GTTTGAACAG ATTAGCTCTG GGGGGAGGGG GTTTCCACAA   3120

TGTGAGGGGG AACCAAGAAA ATTTTAAATA CAGTGTATTT TCCAGCTTCC TGTCTTTACA   3180

CCAAAATAAA GTATTGACAC AAGAG   3205

(2) INFORMATION FOR SEQ ID NO:35:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 761 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

     Met Met Asp Gly Lys Asn Ser Ser Gly Ser Lys Arg Tyr Asn Arg Lys
     1   5   10   15

     Arg Glu Leu Ser Tyr Pro Lys Asn Glu Ser Phe Asn Asn Gln Ser Arg
                     20   25   30

     Arg Ser Ser Ser Gln Lys Ser Lys Thr Phe Asn Lys Met Pro Pro Gln
                 35   40   45

     Arg Gly Gly Gly Ser Ser Lys Leu Phe Ser Ser Ser Phe Asn Gly Gly
             50   55   60

     Arg Arg Asp Glu Val Ala Glu Ala Gln Arg Ala Glu Phe Ser Pro Ala
     65   70   75   80

     Gln Phe Ser Gly Pro Lys Lys Ile Asn Leu Asn His Leu Leu Asn Phe
                     85   90   95

     Thr Phe Glu Pro Arg Gly Gln Thr Gly His Phe Glu Gly Ser Gly His
                     100   105   110

     Gly Ser Trp Gly Lys Arg Asn Lys Trp Gly His Lys Pro Phe Asn Lys
                 115   120   125

     Glu Leu Phe Leu Gln Ala Asn Cys Gln Phe Val Val Ser Glu Asp Gln
             130   135   140

     Asp Tyr Thr Ala His Phe Ala Asp Pro Asp Thr Leu Val Asn Trp Asp
     145   150   155   160

     Phe Val Glu Gln Val Arg Ile Cys Ser His Glu Val Pro Ser Cys Pro
                     165   170   175

                                   189

```
Ile Cys Leu Tyr Pro Pro Thr Ala Ala Lys Ile Thr Arg Cys Gly His
            180             185             190

Ile Phe Cys Trp Ala Cys Ile Leu His Tyr Leu Ser Leu Ser Glu Lys
            195             200             205

Thr Trp Ser Lys Cys Pro Ile Cys Tyr Ser Ser Val His Lys Lys Asp
    210             215             220

Leu Lys Ser Val Val Ala Thr Glu Ser His Gln Tyr Val Val Gly Asp
225             230             235             240

Thr Ile Thr Met Gln Leu Met Lys Arg Glu Lys Gly Val Leu Val Ala
            245             250             255

Leu Pro Lys Ser Lys Trp Met Asn Val Asp His Pro Ile His Leu Gly
            260             265             270

Asp Glu Gln His Ser Gln Tyr Ser Lys Leu Leu Leu Ala Ser Lys Glu
            275             280             285

Gln Val Leu His Arg Val Val Leu Glu Glu Lys Val Ala Leu Glu Gln
            290             295             300

Gln Leu Ala Glu Glu Lys His Thr Pro Glu Ser Cys Phe Ile Glu Ala
305             310             315             320

Ala Ile Gln Glu Leu Lys Thr Arg Glu Glu Ala Leu Ser Gly Leu Ala
            325             330             335

Gly Ser Arg Arg Glu Val Thr Gly Val Val Ala Ala Leu Glu Gln Leu
            340             345             350

Val Leu Met Ala Pro Leu Ala Lys Glu Ser Val Phe Gln Pro Arg Lys
            355             360             365

Gly Val Leu Glu Tyr Leu Ser Ala Phe Asp Glu Glu Thr Thr Glu Val
    370             375             380

Cys Ser Leu Asp Thr Pro Ser Arg Pro Leu Ala Leu Pro Leu Val Glu
385             390             395             400

Glu Glu Glu Ala Val Ser Glu Pro Glu Pro Glu Gly Leu Pro Glu Ala
            405             410             415

Cys Asp Asp Leu Glu Leu Ala Asp Asp Asn Leu Lys Glu Gly Thr Ile
            420             425             430

Cys Thr Glu Ser Ser Gln Gln Glu Pro Ile Thr Lys Ser Gly Phe Thr
            435             440             445

Arg Leu Ser Ser Ser Pro Cys Tyr Tyr Phe Tyr Gln Ala Glu Asp Gly
    450             455             460
```
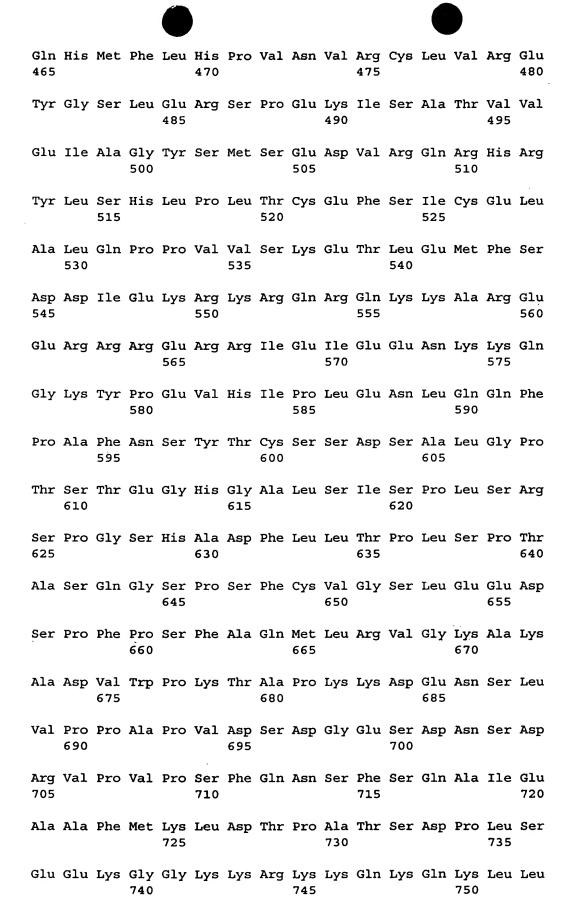
190

Gln His Met Phe Leu His Pro Val Asn Val Arg Cys Leu Val Arg Glu
465   470   475   480

Tyr Gly Ser Leu Glu Arg Ser Pro Glu Lys Ile Ser Ala Thr Val Val
                485   490   495

Glu Ile Ala Gly Tyr Ser Met Ser Glu Asp Val Arg Gln Arg His Arg
            500   505   510

Tyr Leu Ser His Leu Pro Leu Thr Cys Glu Phe Ser Ile Cys Glu Leu
        515   520   525

Ala Leu Gln Pro Pro Val Val Ser Lys Glu Thr Leu Glu Met Phe Ser
        530   535   540

Asp Asp Ile Glu Lys Arg Lys Arg Gln Arg Gln Lys Lys Ala Arg Glu
545   550   555   560

Glu Arg Arg Arg Glu Arg Arg Ile Glu Ile Glu Glu Asn Lys Lys Gln
                565   570   575

Gly Lys Tyr Pro Glu Val His Ile Pro Leu Glu Asn Leu Gln Gln Phe
            580   585   590

Pro Ala Phe Asn Ser Tyr Thr Cys Ser Ser Asp Ser Ala Leu Gly Pro
        595   600   605

Thr Ser Thr Glu Gly His Gly Ala Leu Ser Ile Ser Pro Leu Ser Arg
    610   615   620

Ser Pro Gly Ser His Ala Asp Phe Leu Leu Thr Pro Leu Ser Pro Thr
625   630   635   640

Ala Ser Gln Gly Ser Pro Ser Phe Cys Val Gly Ser Leu Glu Glu Asp
            645   650   655

Ser Pro Phe Pro Ser Phe Ala Gln Met Leu Arg Val Gly Lys Ala Lys
        660   665   670

Ala Asp Val Trp Pro Lys Thr Ala Pro Lys Lys Asp Glu Asn Ser Leu
        675   680   685

Val Pro Pro Ala Pro Val Asp Ser Asp Gly Glu Ser Asp Asn Ser Asp
    690   695   700

Arg Val Pro Val Pro Ser Phe Gln Asn Ser Phe Ser Gln Ala Ile Glu
705   710   715   720

Ala Ala Phe Met Lys Leu Asp Thr Pro Ala Thr Ser Asp Pro Leu Ser
            725   730   735

Glu Glu Lys Gly Gly Lys Lys Arg Lys Lys Gln Lys Gln Lys Leu Leu
        740   745   750

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```
Phe Ser Thr Ser Val Val His Thr Lys
        755                 760
```

(2) INFORMATION FOR SEQ ID NO:36:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 42 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```
Cys Pro Ile Cys Leu Tyr Pro Pro Thr Ala Ala Lys Ile Thr Arg Cys
1               5                   10                  15

Gly His Ile Phe Cys Trp Ala Cys Ile Leu His Tyr Leu Ser Leu Ser
            20              25                  30

Glu Lys Thr Trp Ser Lys Cys Pro Ile Cys
            35              40
```

(2) INFORMATION FOR SEQ ID NO:37:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 41 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
Cys Pro Ile Cys Leu Glu Leu Ile Lys Glu Pro Val Ser Thr Lys Cys
1               5                   10                  15

Asp His Ile Phe Cys Lys Phe Cys Met Leu Lys Leu Leu Asn Gln Lys
            20              25                  30

Lys Gly Pro Ser Gln Cys Pro Leu Cys
            35              40
```

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(2) INFORMATION FOR SEQ ID NO:38:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 44 amino acids
     (B) TYPE: amino acid
     (C) STRANDEDNESS:
     (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Cys Pro Ile Cys Leu Glu Leu Leu Lys Glu Pro Val Ser Ala Asp Cys
1   5   10   15

Asn His Ser Phe Cys Arg Ala Cys Ile Thr Leu Asn Tyr Glu Ser Asn
            20   25   30

Arg Asn Thr Asp Gly Lys Gly Asn Cys Pro Val Cys
            35   40

(2) INFORMATION FOR SEQ ID NO:39:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 40 amino acids
     (B) TYPE: amino acid
     (C) STRANDEDNESS:
     (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Cys Ala Phe Cys His Ser Val Leu His Asn Pro His Gln Thr Gly Cys
1   5   10   15

Gly His Arg Phe Cys Gln Gln Cys Ile Arg Ser Leu Arg Glu Leu Asn
            20   25   30

Ser Val Pro Ile Cys Pro Val Asp
            35   40

(2) INFORMATION FOR SEQ ID NO:40:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 45 amino acids
     (B) TYPE: amino acid
     (C) STRANDEDNESS:
     (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Cys Pro Ile Cys Met Glu Ser Phe Thr Glu Glu Gln Leu Arg Pro Lys
1   5   10   15

```
Leu Leu His Cys Gly His Thr Ile Cys Arg Gln Cys Leu Glu Lys Leu
            20              25              30

Leu Ala Ser Ser Ile Asn Gly Val Arg Cys Pro Phe Cys
            35              40              45
```

(2) INFORMATION FOR SEQ ID NO:41:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 44 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```
Cys Pro Arg Cys Lys Thr Thr Lys Tyr Arg Asn Pro Ser Leu Lys Leu
1               5               10              15

Met Val Asn Val Cys Gly His Thr Leu Cys Glu Ser Cys Val Asp Leu
            20              25              30

Leu Phe Val Arg Gly Ala Gly Asn Cys Pro Glu Cys
            35              40
```

(2) INFORMATION FOR SEQ ID NO:42:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 44 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```
Cys Pro Arg Cys Lys Thr Thr Lys Tyr Arg Asn Pro Ser Leu Lys Leu
1               5               10              15

Met Val Asn Val Cys Gly His Thr Leu Cys Glu Ser Cys Val Asp Leu
            20              25              30

Leu Phe Val Arg Gly Ala Gly Asn Cys Pro Glu Cys
            35              40
```

(2) INFORMATION FOR SEQ ID NO:43:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 39 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
Cys Val Leu Cys Gly Gly Tyr Phe Ile Asp Ala Thr Thr Ile Ile Glu
1               5               10              15

Cys Leu His Phe Ser Cys Lys Thr Cys Ile Val Arg Tyr Leu Glu Thr
            20              25              30

Ser Lys Tyr Cys Pro Ile Cys
        35
```

(2) INFORMATION FOR SEQ ID NO:44:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 40 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```
Cys Ala Ile Cys Leu Asp Glu Tyr Glu Asp Gly Asp Lys Leu Arg Ile
1               5               10              15

Leu Pro Cys Ser His Ala Tyr His Cys Lys Cys Val Asp Pro Trp Leu
            20              25              30

Thr Lys Lys Thr Cys Pro Val Cys
        35              40
```

(2) INFORMATION FOR SEQ ID NO:45:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 41 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```
Cys Thr Ile Cys Tyr Glu Asn Pro Ile Asp Ser Val Leu Tyr Met Cys
1               5               10              15
```

195

A: 149107(UROC014P.DOC)

```
Gly His Met Cys Met Cys Tyr Asp Cys Ala Ile Glu Gln Trp Arg Gly
         20                  25                  30

Val Gly Gly Gly Gln Cys Pro Leu Cys
     35                  40
```

(2) INFORMATION FOR SEQ ID NO:46:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```
AACAGCTATG ACCCTGAGGA                                         20
```

(2) INFORMATION FOR SEQ ID NO:47:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 24 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```
AAGCCCCAAG CCCAGAGACA AGAT                                    24
```

(2) INFORMATION FOR SEQ ID NO:48:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 253 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```
GGCAGGGGCT TGTGACTCTA AGATGGCTTC ATTCACATGC CTAGGGCCTC AGTAGGATGA    60

CTGGCATGGC CCTGGAAAAC TGCGAAGTCT TCTCTCTGTG CAAACTTTCA CCTGGACTTT   120

TTATATGATT CTGGAAGTAT TCCAAGAAGG CAAAAGTAAA AACTGCAAAG CGTCTTAAAA   180

TAGAAGTTCA GAAGCCACAT TATATCACTT CTGTTGCATT CTATCAAAGC AAGTCACAAG   240

CCCCTGCCAA TCA                                                      253
```

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(2) INFORMATION FOR SEQ ID NO:49:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 183 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CACACACTCC CCCATTCTGA GCCCCAAGAG GCTCATCCCT AAGGATGTCC AGAGATCCAA   60

GTGCAGAAGG AGAATGTGGT GAGGCTATTT ATTCCCCCAG TGCCTTCCCT GCTGGGCTAT   120

GGATGAACAG TGGCTGACTT CATCTAGGAA AGAGCTATGG CTTCTGTCTC CTGGAGCTCA   180

CCA   183

(2) INFORMATION FOR SEQ ID NO:50:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 21 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TGCAAACTTT CACCTGGACT T   21

(2) INFORMATION FOR SEQ ID NO:51:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 24 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTTGTGACTT GCTTTGATAG AATG   24

(2) INFORMATION FOR SEQ ID NO:52:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TGTCCAGAGA TCCAAGTGCA GAAGG   25

(2) INFORMATION FOR SEQ ID NO:53:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 25 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GAGCTCCAGG AGACAGAAGC CATAG   25

(2) INFORMATION FOR SEQ ID NO:54:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACATTGAAGC ACTCCGCGAC   20

(2) INFORMATION FOR SEQ ID NO:55:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

AGAGTGGCAG CAACCAAGCT   20

198